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FIG. 1








1  
CCG CTC ACA TTG GGA TTC GTC ATT CTT CTT CTA AAA CCC GCA AAA TTT CTC CAT TTC TAC  
61  
CAA AAA TAT CCA ACT TTT ACT TTT CTT TCC TGT GAA ATT ATC TGC TCA AAT CTT TGG TTC  
121  
CTG ACG GAG ATG GCG GCG ATT TCA GGC ATC TCC TCT GGT ACG TIG ACG ATT TCA CGG CCT  
M A A I S G I S S G T L T I S R P  
181  
TTG GTT ACT CTT CGA CGC TCT AGA GCC GCC GTT TCG TAC AGC TCC TCT CAC CGA TTG CTT  
L V T L R R S R A A V S Y S S S H R L L  
241  
CAT CAT CTT CCT CTC TCT TCT CGT CGT CTG CTA TTA  AAC AAT CAT CGA GTC CAA GCA  
H H L P L S S R R L L L R N N H R V O A  
301  
ACG ATT TTG CAA GAC GAT GAA GAG AAA GTG GTG GTG GAG GAA TCG TTT AAA GCC GAG ACT  
T I L Q D D E E K V V V E E S F K A E T  
361  
TCT ACT GGT ACA GAA CCA CTT GAG GAG CCA AAT ATG AGT TCT TCT TCA ACT AGT GCT TTT  
S T G T E P L E E P N M S S S S T S A F  
421  
GAG ACA TGG ATC ATC AAG CTT GAG CAA GGA GTG AAT GTT TTC CTT  GAC TCG GTT ATT  
E T W I I K L E Q G V N V F L T D S V I  
481  
AAG ATA CTT GAC ACT TTG TAT CGT GAC CGA AGA TAT GCA AGG TTC TTT GTT CTT GAG ACA  
K I L D T L Y R D R T Y A R F F V L E T  
541  
ATT GCT AGA GTG CCT TAT TTT  GCG TTT ATG TCT GTG CTA CAT ATG TAT GAG ACC TTT GGT  
I A R V P Y F A F M S V L H M Y E T F G  
601  
TGG TGG AGG AGA GCA GAT TAT TTG AAA GTA CAC TTT GCT GAG AGC TGG AAT GAA ATG CAT  
W W R R A D Y L K V H F A E S W N E M H  
661  
CAC TTG CTC ATA ATG GAA  GAA TTG GGT GGA AAT TCT TGG TGG TTT GAT CGT TTT CTG GCT  
H L L I M E E L G G N S W W F D R F L A  
721  
CAG CAC ATA GCA ACC TTC TAC TAC TTC ATG ACA GTG TTC TTG TAT ATC TTA AGC CCT AGA  
Q H I A T F Y Y F M T V F L Y I L S P R  
781  
ATG GCA TAT CAC TTT TCG GAA TGT GTG GAG AGT CAT GCA TAT GAG ACT TAT GAT AAA TTT  
M A Y H F S E C V E S H A Y E T Y D K F  
841  
CTC AAG GCC AGT GGA  GAG GAG TTG AAG AAT ATG CCT GCA CCG GAT ATC GCA GTA AAA TAC  
L K A S G E E L K N M P A P D I A V K Y  
901  
TAT ACG GGA GGT GAC TTG TAC TTA TTT  GAT GAG TTC CAA ACA TCA AGA ACT CCC AAT ACT  
Y T G G D L Y L F D E F Q T S R T P N T  
961  
CGA AGA CCA GTA ATA  GAA AAT CTA TAC GAT GTG TTT GTG AAC ATA AGA GAT GAT GAA GCA  
R R P V I E N L Y D V F V N I R D D E A  
1021  
GAA CAC TGC AAG ACA ATG AGA GCT TGT CAG ACT CTA GGC AGT CTG CGT TCT CCA CAC TCC  
E H C K T M R A C Q T L G S L R S P H S  
1081  
ATT TTA GAT GAT GAT GAT ACT GAA GAA GAA TCA GGG TGT GTT GTT CCT GAG GAG GCT CAT  
I L D D D D T E E E S G C V V P E E A H  
1141  
TGC GAA GGT ATT GTA GAC TGC CTC AAG AAA TCC ATT ACA AGT TAA TAA ATT AGA AAG TAA  
C E G I V D C L K K S I T S  
1201  
ACT AAA AAA GAT TAT TTG TAT CAG CTC ATG AAC AAT AGA TAT AAT CCC ATA TAC TTG GGA  
1261  
ATA AAG GAA TAA TGT GAA ATT CCC ATC GTT GTG CTA GTG TGT GAG AGA ATC AAA TAC CCT  
1321  
AAT GAT GTA AAT GTA CTT TGA TGA GCT TAA GTC GTT GTA GAC CAT TTT ATC AAA AAA AAA  
1381  
AAA AAA AAA AAA AAA A

FIG. 2

IMM : 111 FLTDSVIKILDTRYDRTYA-REEVLEELTARVPAFAFMSVLEHMYETFGWRRRADYLVKVFH 169  
 + T +++I L+ R Y R +LET+A VP +LH+ + + ++K  
 AOX : 136 YRTVKLLRIPTDLFFKRRYGCRAIMMLEENVAAPGMVGGMELHLRSLRKQQSGGWIKALL 195  
  
 IMM : 170 AESWNEMHLLIMEELGGSWWFDRFELAQHHAPEVFMVMEINILSPRMAYHFSECVES 229  
 E+ NE HL+ M EL W++R L + ++ LYILSP++A+ +E  
 AOX : 196 EEAENERMHLMTMVEL-VKPKWYERHIAVAVCGVDENAFEEHSPKVAHRIVGYLEEE 254  
  
 IMM : 230 AYETYDKFLK-ASGEELKNMPAPDIAVKYYTGGDLLYLFDEFQTSRTPNTRRPVIENTLYDV 288  
 A +Y ++LK ++N+PAP IA+ Y+ R P L DV  
 AOX : 255 AIHSYTEYKDLKLESGAIENVPAPAIADYW-----RLPKDARLKDV 295  
  
 IMM : 289 FVNIRDDEAEH 299  
 IR DEA H  
 AOX : 296 ITVIRADEAHH 306

## FIG. 3A

T 1 MAISISAMSFGTSVSSYSFCFRARSFEKSSVLCNSQNPCRFSNVFP.IRKSDGASRCSVSR  
P 1 MAISISAMSFRTSVSS.....SY..SAFLCNSKNPFCLNSLFS.LRNSHRTFQPSLSR  
A 1 MA.AISGISSGTLTIS.....RPLVTLRRSRAAVSYSSSHRLLHHLPLSSRRLLLR  
consensus

1 MA ISamS T S L S S lr 1 R

T 60 KSCRVRATLLQENEEVVVEKSFAPKSFDPNVGGGSGXKPPDDSSS.NGLEKWVIKLEQS  
P 51 KSSRVTRATLLKENEEVVVEKSFAPKSFPGNVGGGNNGEPPDNSSS.NGLEKWVIKIEQS  
A 51 NNHRVQATILQDDEEKVVVEESFKAEL...TSTGTEPLEEPNMSSSSTSAFETWIIKLEQG  
consensus

61 RV ATIL e EE VVVE SF G P SSS g E WVIKIEQ

T 119 VNILLTDSVIKILDTLYHNRNYARFFVLETIARVPYFAFISVLHMYESFGWRRADYMKV  
P 110 VNIFLTDSVIKILDTLYHNRNYARFFVLETIARVPYFAFISVLHLYESFGWRRADYLVK  
A 108 VNVFLTDSVIKILDTLYRDRYARFFVLETIARVPYFAFMSVLHMYETFGWRRADYLVK  
consensus

121 VNI LTDSVIKILDTLYh R YARFFVLETIARVPYFAFISVLHLYESFGWRRADYLVK

T 179 HFAESWNEMHHLLIMEELGCGNAWWFDRFLAQHIAIFYFMTVLMYALSPRMAYHFSECVE  
P 170 HFAESWNEMHHLLIMEELGCGNAWWFDRFLAQHIAIFYFMTVSMYALSPRMAYHFSECVE  
A 168 HFAESWNEMHHLLIMEELGCGNSWWFDRFLAQHIATFYFMTVFLYILSPRMAYHFSECVE  
Consensus

181 HFAESWNEMHHLLIMEELGCGN WWFDRFLAQHIA FYYFMTV mY LSPRMAYHFSECVE

T 239 SHAYETYDKFIKDQGEELKNLPAPKIAVDYYTGGDLYLDEFQTSREPNTTRPKIDNLYD  
P 230 HHAYETYDKFIKDQEAELKKLPAPKIAVSYYTGGDLYLDEFQTSREPNTTRPKIDNLYD  
A 228 SHAYETYDKFLKASGEELKNMPAPDIAVKYYTGGDLYLDEFQTSRTPTNTRPVIENTLYD  
Consensus

241 HAYETYDKfIK ELK lPAP IAV YYTGGDLYLDEFQTSR PNTRRP IdNLYD

T 299 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTD.PCDDSEDDTGCSVP.QADCIGIVDCIKK  
P 290 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTN.PCDESEDDPGCSVP.QADCVGIVDCITK  
A 288 VFVNIRDDEAEHCKTMRACQTLGSLRSPHSILDDDDTEESGCVVPEEAHCEGIVDCCLKK  
Consensus

301 VFmNIRDDEAEHCKTMkACQT GSLRSPHT DdsEdd GC VP A C GIVDCI K

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## FIG. 3B

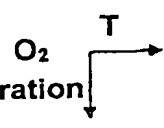
T 357 SVTDTQVTKR

P 348 SVADPNVGRR

A 348 SITS.....

Consensus

361 Sv



**membranes**      **E. coli**



FIG. 4B